

GenCore version 5.1.6  
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# OM nucleic - nucleic search, using sw model

Run on: August 19, 2003, 09:37:35 ; Search time 6189 Seconds  
(without alignments)  
12039.761 Million cell updates/sec

Title: US-09-494-297-1  
Perfect score: 2274  
Sequence: 1 atgaataaaacaagtttc.....ggataagaataacatgactag 2274

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32997241 seqs, 16383922548 residues  
Total number of hits satisfying chosen parameters: 65994482

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Pending\_Patents\_NA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pna/PCRRUS\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pna/PCRRUS\_COMB.seq.old.\*
- 3: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pna/US080\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pna/US083\_COMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pna/US084\_COMB.seq.\*
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- 13: /cgn2\_6/ptodata/1/pna/US088\_COMB.seq.\*
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- 16: /cgn2\_6/ptodata/1/pna/US091\_COMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pna/US092A\_COMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pna/US092B\_COMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pna/US093A\_COMB.seq.\*
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- 21: /cgn2\_6/ptodata/1/pna/US094\_COMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pna/US095A\_COMB.seq.\*
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- 24: /cgn2\_6/ptodata/1/pna/US095C\_COMB.seq.\*
- 25: /cgn2\_6/ptodata/1/pna/US095D\_COMB.seq.\*
- 26: /cgn2\_6/ptodata/1/pna/US096A\_COMB.seq.\*
- 27: /cgn2\_6/ptodata/1/pna/US096B\_COMB.seq.\*
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- 38: /cgn2\_6/ptodata/1/pna/US099A\_COMB.seq.\*
- 39: /cgn2\_6/ptodata/1/pna/US099B\_COMB.seq.\*
- 40: /cgn2\_6/ptodata/1/pna/US099C\_COMB.seq.\*
- 41: /cgn2\_6/ptodata/1/pna/US099D\_COMB.seq.\*
- 42: /cgn2\_6/ptodata/1/pna/US099E\_COMB.seq.\*
- 43: /cgn2\_6/ptodata/1/pna/US099F\_COMB.seq.\*

Result	No.	Score	Query Match	Length	ID	Description
1	2274	100.0	2274	21	US-09-494-297-1	Sequence 1, Appl1
2	720.8	31.7	2229	21	US-09-494-297-3	Sequence 3, Appl1
3	60	2.6	1095	44	US-10-015-127-1938	Sequence 1938, Ap
4	58.8	2.6	535	31	US-09-705-926-16876	Sequence 16876, A

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C	10	57.2	2.5	1288	44	US-10-266-090-314	49	Sequence 314, App A
C	11	56.6	2.5	4677	1	PCT-US99-26796-392	1	Sequence 392, App A
C	12	56.6	2.5	4677	2	PCT-US99-26796-392	2	Sequence 392, App A
C	13	56.6	2.5	33392	29	US-09-662-254-27	29	Sequence 27, App1
C	14	56.6	2.5	33392	29	US-09-662-254-27	29	Sequence 27, App1
C	15	56	2.5	12205	49	US-10-266-090-323	33	Sequence 323, App A
C	16	56	2.5	11922	1	PCT-US99-26796-320	1	Sequence 320, App A
C	17	56	2.5	11922	2	PCT-US99-26796-320	2	Sequence 320, App A
C	18	55.6	2.4	591	28	US-09-654-617-428715	15	Sequence 428, App A
C	19	55.6	2.4	591	29	US-09-654-617-11158	15	Sequence 1158, App A
C	20	55.6	2.4	591	30	US-09-684-016-428715	15	Sequence 428, App A
C	21	55.6	2.4	591	53	US-10-437-963-21828	15	Sequence 218, App A
C	22	55.4	2.4	570	25	US-09-665-306-26113	13	Sequence 261, App A
C	23	55.4	2.4	636	21	US-09-406-292A-4371	13	Sequence 437, App A
C	24	55	2.4	1056	102	US-60-475-871-1807	102	Sequence 1807, App A
C	25	55	2.4	1115	49	US-10-266-090-20483	49	Sequence 20483, App A
C	26	53.8	2.4	1362	49	US-10-282-122A-16609	49	Sequence 16609, App A
C	27	53.8	2.4	5940	1	PCT-US99-26796-238	1	Sequence 238, App A
C	28	53.8	2.4	5940	2	PCT-US99-26796-238	2	Sequence 238, App A
C	29	53.8	2.4	10721	67	US-60-068-228-325	67	Sequence 325, App A
C	30	53.8	2.4	10736	50	US-60-038-081-318	50	Sequence 318, App A
C	31	53.8	2.4	10736	58	US-60-046-933-322	58	Sequence 323, App A
C	32	53.6	2.4	1748	31	US-09-620-392-14063	31	Sequence 14063, App A
C	33	53.6	2.4	1748	37	US-09-702-134-46187	37	Sequence 46187, App A
C	34	53.6	2.4	1748	34	US-09-815-264-78501	34	Sequence 78501, App A
C	35	53.6	2.4	1748	68	US-60-144-351-2763	68	Sequence 2763, App A
C	36	53.4	2.3	7218	9	US-08-466-194-14	9	Sequence 14, App1
C	37	53.2	2.3	1575	34	US-09-543-681A-615	34	Sequence 615, App A
C	38	53	2.3	494	33	US-09-785-276B-10012	33	Sequence 10012, App A
C	39	53	2.3	335913	32	US-09-754-853A-3	32	Sequence 2, App1
C	40	53	2.3	335913	32	US-09-754-853A-3	32	Sequence 3, App1
C	41	53	2.3	335913	35	US-09-855-768-5	35	Sequence 5, App1
C	42	52.8	2.3	8210	48	US-10-321-613-243	48	Sequence 243, App A
C	43	52.4	2.3	989	20	US-09-397-761A-2729	20	Sequence 2729, App A
C	44	52.4	2.3	989	35	US-09-838-601-2729	35	Sequence 2729, App A
C	45	52.4	2.3	6106	49	US-10-257-166-113	49	Sequence 113, App A

## ALIGNMENTS

```

RESULT 1
US-09-494-297-1
: Sequence 1, Application US/09494297
: GENERAL INFORMATION:
: APPLICANT: POBIELESKI, ANDREAS
: TITLE OF INVENTION: COLLAGEN-BINDING PROTEINS FROM STREPTOCOCCUS PYOGENES
: FILE REFERENCE: P06628US0/BAS
: CURRENT APPLICATION NUMBER: US/09/494,297
: CURRENT FILING DATE: 2000-01-31
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 2274
: TYPE: DNA
: ORGANISM: Streptococcus pyogenes
US-09-494-297-1

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Query Match	100.0%;	Score 2274;	DB 21;	Length 2274;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2274;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 ATGAAAAAACAAGGTTCCAAATAGCTTAATCTTAATACGAAGGGATTAGT 60  
Db 1 ATGAAAAAACAAGGTTCCAAATAGCTTAATCTTAATACGAAGGGATTAGT 60  
QY 61 AAAAAGTCAAACGATTACTGTCACTTAGCGSAGCTTTTAATGATCTTCGCTTG 120  
|||||

D	b	61	AAAACTCAAAACGATTACTGCTACCTTAGGGGAGCTTTTAAATGATCTTCGCTTG	120
O	y	121	GTAACTTCATGGTGGTGCTAAGACTGTTTTGGTTAGTAAGAACTCCGAGGCCAAAC	180
D	b	121	GTAACTTCATGGTGGTGCTAAGACTGTTTTGGTTAGTAAGAACTCCGAGGCCAAAC	180
O	y	181	GCAATAATCCAGATTCAAGTTCGGAAATACAGATGTGGATATGAATCTTATCTAAGA	240
D	b	181	GCAATAATCCAGATTCAAGTTCGGAAATACAGATGTGGATATGAATCTTATCTAAGA	240
O	y	241	GGGACATCATTTTAAACAGTTTGAGTAGACACACGATTTAAGGTTAACTTACAGAGA	300
D	b	241	GGGACATCATTTTAAACAGTTTGAGTAGACACACGATTTAAGGTTAACTTACAGAGA	300
O	y	301	AGTAGAACTTATCAAGTTATTTGCTTTAAATTTAAAGAAAGCATTTCTCTCGGATCAGAT	360
D	b	301	AGTAGAACTTATCAAGTTATTTGCTTTAAATTTAAAGAAAGCATTTCTCTCGGATCAGAT	360
O	y	361	AGTAGTGTAAAAAGCTGTATTAATAAACATGATGGAATCTCTACAAAATTTGAGATTAAT	420
D	b	361	AGTAGTGTAAAAAGCTGTATTAATAAACATGATGGAATCTCTACAAAATTTGAGATTAAT	420
O	y	421	GGGATGACCCCTAGATTAACGGGAGATGAGCTAAATCGAAGTTTCGAGCTTTATGAT	480
D	b	421	GGGATGACCCCTAGATTAACGGGAGATGAGCTAAATCGAAGTTTCGAGCTTTATGAT	480
O	y	481	AATGACATCCACAAAATGCCAATGTTATGGAAGCTTGGAAACCTTGATGATCTATC	540
D	b	481	AATGACATCCACAAAATGCCAATGTTATGGAAGCTTGGAAACCTTGATGATCTATC	540
O	y	541	AGAGTTACACAAGAGCGGTATGGTACTATTTCTGATAATGCTCTATTTCTTAATCCAGAT	600
D	b	541	AGAGTTACACAAGAGCGGTATGGTACTATTTCTGATAATGCTCTATTTCTTAATCCAGAT	600
O	y	601	GAAAGTTTAAAAAGGAGTACAGAAAGTAACTGGTAACTACTCTCCATTTATCTTTGATG	660
D	b	601	GAAAGTTTAAAAAGGAGTACAGAAAGTAACTGGTAACTACTCTCCATTTATCTTTGATG	660
O	y	661	CGTCAAGCTTTGAAGCAACTATTTGATCCGAATTTGGCACTAAATGCCAAAACAAGTT	720
D	b	661	CGTCAAGCTTTGAAGCAACTATTTGATCCGAATTTGGCACTAAATGCCAAAACAAGTT	720
O	y	721	CCGAGATGATTTTCAGCTAAGTATTTTGGATGCTGAGGACAAGGAGATTAATATATAA	780
D	b	721	CCGAGATGATTTTCAGCTAAGTATTTTGGATGCTGAGGACAAGGAGATTAATATATAA	780
O	y	781	GGATATCCAAATCTTTGAGTGGTGGTAACTACTACTATAAACCCCAACTCCAGGAGAC	840
D	b	781	GGATATCCAAATCTTTGAGTGGTGGTAACTACTACTATAAACCCCAACTCCAGGAGAC	840
O	y	841	CCACCAATGSCCTCCAAATCAACCTCAACGACTTCAGTACTATATAGAAAGTATGCTATA	900
D	b	841	CCACCAATGSCCTCCAAATCAACCTCAACGACTTCAGTACTATATAGAAAGTATGCTATA	900
O	y	901	GGTATTAATCTTAAATTTGCTTGAAGGTGCAACATTACAGTTGACAGGAGATTAAGTGAAT	960
D	b	901	GGTATTAATCTTAAATTTGCTTGAAGGTGCAACATTACAGTTGACAGGAGATTAAGTGAAT	960
O	y	961	AGTTTCAAGGAGAGGTGTTAGAGATTAATGATTTGGAGAAAGATTTGAACATTAACAAT	1020
D	b	961	AGTTTCAAGGAGAGGTGTTAGAGATTAATGATTTGGAGAAAGATTTGAACATTAACAAT	1020
O	y	1021	GGAATTAATCTTAACTGAATTAATTTCTCAGCTGGTTATAGATGCGAGAGCCAATC	1080
D	b	1021	GGAATTAATCTTAACTGAATTAATTTCTCAGCTGGTTATAGATGCGAGAGCCAATC	1080
O	y	1081	ACTTTTAAAGTTGAAGCTGGCAAGGTGTAATTTATTTGATGGAAAAACAATTTGAAATTT	1140
D	b	1081	ACTTTTAAAGTTGAAGCTGGCAAGGTGTAATTTATTTGATGGAAAAACAATTTGAAATTT	1140
O	y	1141	CCCAATAAAGAGATAGTAGAGCCCTTACTACATAGAAGCATTAATGATTTGGAAGAAATTT	1200
D	b	1141	CCCAATAAAGAGATAGTAGAGCCCTTACTACATAGAAGCATTAATGATTTGGAAGAAATTT	1200



QY	841	CCACCAATGSCCTCCAAATCAACCTCAAAACGCTTAGTACTATTAGAAAGTATGCTATA	900
Db	789	-----AGAGCCCTCGGGCTPAAACCTGAAAAAATATGATAGCTATTATGAAAAATATGCGAA	843
QY	901	GGTGATTACTCTAAATTTGCTTGAAGGTGCACACATTACAGTTGCACGGGGATTAACGTGAAT	960
Db	844	GGTG--ACTGTAAACTCTTAGAGGGACCAACCTTAAAGCTTTCTCAAAATTGAGGAAGT	900
QY	961	AGTTTCAAGCGAGAGGTGTTTAGCGATATGATATTGGAGAAAGAAATTGAACATACAGAT	1020
Db	901	GGTTTTCAGAAAAAGACCTTTCAAAGTAAATAGTTTAGAGAAAACGTGCAATTTACCAAT	960
QY	1021	GGAACTTATACCTTAACTGAATTGAAATTCCTCCAGCTGGTTATAGTATGCACAGCAATC	1080
Db	961	GGGACTTTATACCTTACAGAAAACATCATCTCCAGATGGATATATAAATTGGCGAGCGGAT	1020
QY	1081	ACTTTTAAGTTGAAGTCGGCAAGTGTATCTAT--TATTGATGAGAAAAACAGATTGAA	1130
Db	1021	AAGTTTAAGTAGAGAAATPAAAAAGTATTTATTCGCCAAAAAGAGTTCTTCACGTGAA	1080
QY	1138	AATCCCATTAAGAGATAGTAGAGCTTACCTACAGTACAGTAAAGCATATAATGATTTT--GAA	1190
Db	1081	AATCCAAACAAAGAGTAGACAGAGCATACCTAGTGAAGCGCTATAATGACTTTATGAT	1140
QY	1195	GAATTTAGCGTTTAACTACACAAAACTATGCAAAAAATTTTATATGCAAAAAATAAAAAT	1250
Db	1141	GAAAGAACTACTCGGGTTTAACTCCATACGGAATAATTTCTATTACGTACAAATPAAAGT	1200
QY	1255	GGAGTTACAGAGTTGTCTATTGCTTTAATGACAGATCTTAAATCTCCACAGACTGTGAA	1310
Db	1201	AAAGTTTACAGAGTTGTCTACTGCTTCAAGCTGATTTACATCCACACCTGTGACATAT	1260
QY	1315	GATGCTGGAAAAACATACCTCAGACA--CTTTAACAGAGGAGAGTAAATATACCTGAT	1370
Db	1261	GATAGTGGTAGACATATAATCCAGATACGTAGTACGATGAAAAAGATCAAGTACACACAT	1320
QY	1372	ATTGCAAGTCTGACCTCTTTAATATATCTGTGAACCAAGAGATACCGATCTGCACACT	1430
Db	1321	ACGGAGGATGATGACTTGTTTAAATATCGCTTAAACCCAGAGAGATACAAATCCAGAAAC	1380
QY	1432	TTCTTAAACAATATCAAAAAAGTAATAGAGAAAGGTTACAGGAAAAAGAACACAGCTAT	1490
Db	1381	TTCTTAAAGCACATTTAAAAAAGTATTTAAAAAAGGCTCCAGAAAAAAG-----TGAT	1430
QY	1492	GAGTATAGTGTCTTAACCTGAGACACAAATGGCGTGGCTACTCAGTTAGCAATATATAT	1550
Db	1435	AGCTATATATGATTAACAGAAAAACAGTTTGGCGGCTACTACACTTGCTATCATATAT	1490
QY	1552	TTCACTGATAGTGGTGAATTAGA-----TAAGATPAACTTAAAGACATATCAT	1590
Db	1495	TTTACAGCACTGCTGACTTTAAAAACCTTAAAAACTTATPAAACAATGGGAAAGTTACAT	1550
QY	1600	GGTTTGGAGACATGAATGATAGTACTTTAGCACTTGTCTTAAATCCTGTGAATATACCT	1650
Db	1555	GGATTTGAATGTATGAGATGAAAAAACCTAGCTGTCAAAAAAGAAATTAATTAAGTATGCT	1610
QY	1660	CAAGATATATCTCTCCACAGCTATACGTAACCTTGATTTTCTTTATTCGAAATPACATATAA	1710
Db	1615	CAAAATGGCAATGGCCCTCAACTCAAAATCTTGATTTCTTCGTACCTTAATAATPAGCAAA	1670
QY	1720	TATCAATCTCTTATTTGAAATCAGAGGGATCCAGAAAGTTTATAGTATATATATTCGTATG	1770
Db	1675	GACCAATCTCTTATTTGGACACGAATGCCATCCAGTATGATTTGGTTGACGTATATTCGTATG	1730
QY	1780	GAAATATAAA--AAGAAATTAATACCTGTAACTCATATTTTAACTTACATTGAGAAAAACGGTG	1830
Db	1735	GAAATATAAAAGCAAGAAAGTATTTCCAGTAACCTACACAGTTTGACAGTGAATAAAACAGTA	1790
QY	1837	ACTGTTTACGTGGGTGACAGAACTPAAAGATTTCCATTTTGAATTTGAATTAAAAATATAT	1890
Db	1795	GTGCGTGGATTTGGGAGATPAAACTPAAAGGCTTCATATTTGAATTTGAATTTGAATTAAGATATAA	1850

QY	1897	AAGCAGAGATTGCTTTCCCAACGCTTTAAACACAGATAAACCAAACTCGAATTTAAAGAT	1956
Db	1855	ACTGGACGCGCTATTGTTTAAACGCTTAAACCTATATACTCAAGATTAGTAGCTAAAGAT	1914
QY	1957	GGTAAGACACCATTAATTTAAACATGGGAAAGTTTAAACATCTCAAGTTTACCGAAA	2016
Db	1915	GGGAATATTCTATTTAATCTTAAGCATGTCGACACCATTAAGAATAGAAGATTACCGACG	1974
QY	2017	GGTTATTTCTACCTTGTCAAAGAAAACAGATTCTGAAGGCTTTAAAGTTAAATAGC	2076
Db	1975	GGATATTCTCTTACTCTGAAGAGGCGTAACGCTAAAGGATTATTATAGTAACCGTTGATAAC	2034
QY	2077	CAAGACAGACAAATGCTACAGTTTCAAAAACAGAAATTAACAATGATGAGACCTTGCT	2136
Db	2035	AAATCTTACTCAAGAGCGCACCTACAGTAGATATATACGAAGACCAAAAAAGTCACT	2094
QY	2137	TTTGAAATATATAAAGACCGCTGGTGTCTCTACAGAGTTGATCAAAAGATCAATGGCTAT	2196
Db	2095	TTTGCAAAAACGAAAGAATCTTGTCGCCACCAACTGCTTTGACACACAGATGGGGCTATCTAT	2154
QY	2197	CTACCTTTGATAGTTATCGCTGGATACAGTTTGGGGATCTGGGGAATTTACACAGATPAGG	2256
Db	2155	CTTTGGTGTGTTATTAAGTCTTGCCACTGGGGTTATTTGGTGGCTATTTGGTCGTAAAGGG	2214
QY	2257	ATAAGAAA	2264
Db	2215	TTTAAAAA	2222

```

RESULT 3
US-10-015-127-1938
; Sequence 1938, Application US/10015127
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkley, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof
; FILE REFERENCE: 38-10(15806)B
; CURRENT APPLICATION NUMBER: US/10/015,127
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/252,455
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 14357
; SEQ ID NO 1938
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Sphingomonas elodea
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1095)
; OTHER INFORMATION: unsure at all n locations
US-10-015-127-1938

```

[illegible]

: APPLICANT:     Bynum, Joseph R.  
 : APPLICANT:     La Rosa, Thomas J.  
 : APPLICANT:     Shukla, Hridayabhirraojan  
 : APPLICANT:     De La Pena, Robert C.  
 : APPLICANT:     Bougrl, Olegs

Query Match	2.6%;	Score 58.2;	DB 35;	Length 425;
Best Local Similarity	48.4%;	Pred. No. 0.083;		
Matches 162;	Conservative 0;	Mismatches 173;	Indels 0;	Gaps 0;

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QY 1877 AATGATTTAAATAATTAACGAGATTCCTTCTCAACTGTTAAACGATTAATA 1936
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8 AAAAAAAAAAAAAAAAAAAAAACCAAAATTTAAAAAAAAAAAAAAAAAAATTA 67
QY 1937 CAACCTCGAATTTAAGATGTAAGCAACCATTAATTTAAACATGGGAAAGTTAA 1996
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 AAAAAAAAAAAAAAAAAATTCGAAAAAATAAAAAAAAAAAAAAAAAATTTAAATTTCA 127
QY 1997 CACTTCAGGTTTACAGAGGTTATCTTCTTCTCAACGAAACAGATTCGAGGCT 2056
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 AATTAATTTAGGAAAAAATAAAAAAAAAAAAAAAAAATTTAAAAAATTTAAATTTCA 187
QY 2057 ATAGGTTAAAGTTAAGCAGAGTAGCAATGCTACAGTTTCAAAACAGATTA 2116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 188 AAAAAAGAAAAAATAATTAATTAATAAAAAAAAAATTTAAATTTAAAGAAAAA 247
QY 2117 CAAGTATGACACTGCTTTGAAATTAATTAAGACGCTGTTCTACAGAGTTG 2176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 248 AATTAATAAAACCCCTTTATTTAATTTAAATAAAAAAAAAATTTTAAATAATTTT 307
QY 2177 ATCAAAAGATCAATGCTATCTAGCTTATAGT 2211
Db 308 TAAAAATTAATAATTTTAAAAAATTTAACCTT 342

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## RESULT 7

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US-60-197-872-73058
; Sequence 73058, Application US/60197872
; GENERAL INFORMATION:
; APPLICANT: Bougri, Olegs
; APPLICANT: Byrum, Joseph R.
; APPLICANT: De La Pena, Robert C.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Shukla, Hridayabhiranjan
; TITLE OF INVENTION: Nucleic acid molecules and other molecules associated with
; FILE REFERENCE: 38-21(51892)A
; CURRENT APPLICATION NUMBER: US/60/197,872
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 76255
; SEQ ID NO 73058
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Oryza sativa japonbare
; OTHER INFORMATION: Clone ID: LIB3599-006-Q1-K1-G11
US-60-197-872-73058

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## Query Match

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Best Local Similarity 48.4%; Score 58.2; DB 73; Length 425;
Matches 162; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

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QY 1877 AATGATTTAAATAATTAACGAGATTCCTTCTCAACTGTTAAACGATTAATA 1936
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8 AAAAAAAAAATAAAAAAAAAAACCAAAATTTAAAAAAAAAAAAAAAAAAATTA 67
QY 1937 CAACCTCGAATTTAAGATGTAAGCAACCATTAATTTAAACATGGGAAAGTTAA 1996
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 AAAAAAAAAAAAAAAAAATTCGAAAAAATAAAAAAAAAAAAAAAAAATTTAAATTTCA 127
QY 1997 CACTTCAGGTTTACAGAGGTTATCTTCTTCTCAACGAAACAGATTCGAGGCT 2056
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 AATTAATTTAGGAAAAAATAAAAAAAAAAAAAAAAAATTTAAAAAATTTAAATTTCA 187
QY 2057 ATAGGTTAAAGTTAAGCAGAGTAGCAATGCTACAGTTTCAAAACAGATTA 2116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 188 AAAAAAGAAAAAATAATTAATTAATAAAAAAAAAATTTAAATTTAAAGAAAAA 247
QY 2117 CAAGTATGACACTGCTTTGAAATTAATTAAGACGCTGTTCTACAGAGTTG 2176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 248 AATTAATAAAACCCCTTTATTTAATTTAAATAAAAAAAAAATTTTAAATAATTTT 307
QY 2177 ATCAAAAGATCAATGCTATCTAGCTTATAGT 2211

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Db 308 TAAAAATTAATAATTTTAAAAAATAATTTAACCTT 342

```

## RESULT 8

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US-09-553-094-12310
; Sequence 12310, Application US/09553094
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15503)B
; CURRENT APPLICATION NUMBER: US/09/553,094
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 18831
; SEQ ID NO 12310
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3061-099-Q1-N6-A2
US-09-553-094-12310

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Query Match
Best Local Similarity 47.8%; Score 57.8; DB 25; Length 617;
Matches 164; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

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QY 1811 ATATATTAACTTGAAAAAAGCGTACGCTGTTTACTGCTGACAGAACTAAAGATTCC 1870
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 117 AAAAAAAAAATAATTAATAAAAAAAAAATTTTGGATTTGAATTAANGGAAATTAATAATTTT 176
QY 1871 ATTTGAATTTGAATTAATAATAATTAACCAAGATTCCTTCTCAACTGTTAAACAG 1930
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 177 ATATTAAATTTAAAAAATAAAAAAAAAAAAAAAAAATTTAAATTAATAAAAAAAAAAGAA 236
QY 1931 ATTAACAACCTCGAATTTAAGATGTAAGCAACCATTAATTTAAACATGGGAAA 1990
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 237 AAAAAAAGATAATTAATAAAAAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 296
QY 1991 GTTTACACTGCTGAGGTTTACGAGGTTATCTTCTGTCAGAAAGACGATTCTG 2050
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 297 AATTAATAAGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAGAAATA 356
QY 2051 AAGGCTATAAGTTAAGTTAATGAGCAAGAGTAGCAATGCTACAGTTTCAAAAACAG 2110
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 357 AAGAAAAAATAATTAATAAAAAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 416
QY 2111 GAATTAACAAGTATGACACTGCTTTGAAAAATTAATAAGA 2153
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 417 AAAAAAGATAATTAATAAAAAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 459

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## RESULT 9

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US-10-015-127-2421
; Sequence 2421, Application US/10015127
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Spingomonas elodea genome sequences and uses thereof
; FILE REFERENCE: 38-10(15806)B
; CURRENT APPLICATION NUMBER: US/10/015,127
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/252,455
; NUMBER OF SEQ ID NOS: 14357
; SEQ ID NO 2421
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Spingomonas elodea
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1368)

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APPLICANT: GOFF, STEPHEN  
APPLICANT: BONAN, CAROLINE  
APPLICANT: COLBERT, MICHELLE  
APPLICANT: WANG, RONG-LIN  
TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE

:  
 :  
 : CURRENT APPLICATION NUMBER: PCT/US99/26796  
 : CURRENT FILING DATE: 1999-11-05  
 : NUMBER OF SEQ. ID NOS: 420  
 : SOFTWARE: Patentln Ver. 2.1  
 : SEQ. ID NO 392  
 : LENGTH: 4677  
 : TYPE: DNA  
 : ORGANISM: Plasmodium falciparum  
 : PCT-US99-26796-392



Query Match 2.5%; Score 56.6; DB 1; Length 4677;  
 Best Local Similarity 43.5%; Pred. No. 0.37;  
 Matches 416; Conservative 0; Mismatches 529; Indels 12; Gaps 3;

QY 1084 TTTAAGCTTAAGCTGCGCAAGTGTATCTATTATGATGGAACAGATTGAAATCCC 1143  
 DB 3256 TCTGATTTAAAGATCTTGAAGAGATATTTAAAGAGCTAAAGAAATCAAGAACTT 3315  
 QY 1144 AATAAGAGATAGTAGACCTTACTCTGTAAGACATATATGTTTGAAGATTAGC 1203  
 DB 3316 GAAAGTCAATTTTATAGAGATTTAAAGAACTTTGAAGACAGATATTTTGA 3375  
 QY 1204 GTTTAACTACACAAAATCTATGCAAAATTTATATGCAAAAATTAATAATGAACTTCA 1263  
 DB 3376 GAGAAAAAAGAAATAGAAAAAGATCATTTTGAAAAATTCAGAGAGAGCTGAAGAAATA 3435  
 QY 1264 CAGGTGCTATTTGCTTTAATGCAAGATCTAAATCTCCACAGACTCTGAGATGTGGG 1323  
 DB 3436 AAGATCTTGACAGATATTTAAAGAGATCTTCAATTAAGATTGAAGAAATA 3495  
 QY 1324 AAAACATGACTCCAGCTTTTACACAGAGAGTAATAATACACTCATATTGCAAGTCT 1383  
 DB 3496 AATTTAGAGAGACTACGAAATTTAAAGAGAGGTAGAA-----CATATATTAAGTGT 3549  
 QY 1384 GACCTCTTTAATATCTGTGAACCAAGAGATACCGATCTGACACTTTCTTAAACAT 1443  
 DB 3550 GATGCGCATTTAAAGGTTTGGAAGAGATGATTTAGAGAGATGATTTTAAAGGA 3609  
 QY 1444 ATCAAAAAATTAATGCAAGGTTTACAGGAAAAAGACAGCTTATGATAGTGT 1503  
 DB 3610 AGTATTTAGACATGTTAAAGGAGATGTGAATTTAGGGATATGATTAAGAAAGTTTA 3669  
 QY 1504 CTAACTGAGACAAATTCGTGGCGGTACTCAGTTACCATATATTTTCCACTGATAGT 1563  
 DB 3670 GAAGATGTAAACAGCAAACTTTGGAAGAGAGTGAATCTTAAAGATGTTTATCTAGT 3729  
 QY 1564 GCTGAATTAAGATTAAGTAACTAAAGACTATCATGTTTGGAGACATGAATGATAGT 1623  
 DB 3730 GC---ATTAGCATGTAGTAAAGAACAAATGAAGAAAGAAAGAAAGCTCAAGACCTAAA 3786  
 QY 1624 ACTTTAGCAGTGTCTAAATCTTGTGAATAGCCTCAAGATAGTAACTCCACAGCTA 1683  
 DB 3787 TTGGAAGAGATATTAATAAGAGAGGTTTAAAGAACCAAGAAAGAAATTAACAAA 3846  
 QY 1684 ACTGACCTGATTTCTTATTCGAAATTAACATTAATATCATCTCTTATTTGAACTCAG 1743  
 DB 3847 AAGAAAGTAAAGTTTGTATTAAGATTAAGAACCAAGATGAATAGTAAAGTTGAA 3906  
 QY 1744 TGGCATCCAGAGATTTAGTTGATATATTCGTATGGAAGATTAAGAAAGATTAATCT 1803  
 DB 3907 ATGAAGATGAAGATTAAGATTAAGATTAAGAAAGATTAAGAAAGATTAAGAAAG 3966  
 QY 1804 GTAACTCATTAATTAACATTGAGAAAAAGCGTACGTGTTTACGTGTGACAGAACTAAA 1863  
 DB 3967 GATTAAGTTGAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 4026  
 QY 1864 GATTTCATTTGAAATTTGAATTAATAATTAAGCAAGATTTGCTTTTCAAGCTGT 1923  
 DB 4027 GACAAAGATGAAGTTTATGATTTAATGTCCAAAAAGAGAGACATG---AAAAGTT 4083  
 QY 1924 AAAACAGATTAAGCAAACTCGAATTTAAAGATTAAGATTAAGCAAACTTAATTAACAT 1983  
 DB 4084 AAGAGAAAAAGAAAAATTAAGAAAAAGTTGAAGAGAGTTAGTGTCTTAAAGAA 4143  
 QY 1984 GGGGAAAGTTTAACTCTCAAGTTTACCAAGAGTTATTTCTTACCTGTCAAGAA 2040  
 DB 4144 CAGCTAGACGAATTAAGAAATATGTTCAAAAATTTGATTAAGAGATTGATTAAGAA 4200

RESULT 12  
 PCT-US99-26796-392  
 : Sequence 392, Application PC/TUS9926796

GENERAL INFORMATION:  
 : APPLICANT: United States Government as Represented by the  
 : APPLICANT: Secretary of the Navy  
 : TITLE OF INVENTION: Chromosome 2 Sequence of Human Malaria Parasite  
 : TITLE OF INVENTION: Plasmodium Falciparum and Proteins of Said  
 : TITLE OF INVENTION: Chromosome Useful in Anti-malarial Vaccines and  
 : FILE REFERENCE: Diagnostic Reagents  
 : CURRENT APPLICATION NUMBER: PCT/US99/26796  
 : CURRENT FILING DATE: 1999-11-05  
 : NUMBER OF SEQ. ID NOS: 420  
 : SOFTWARE: PatentIn Ver. 2.1  
 : SEQ. ID NO 392  
 : LENGTH: 4677  
 : TYPE: DNA  
 : ORGANISM: Plasmodium falciparum  
 : PCT-US99-26796-392

Query Match 2.5%; Score 56.6; DB 2; Length 4677;  
 Best Local Similarity 43.5%; Pred. No. 0.37;  
 Matches 416; Conservative 0; Mismatches 529; Indels 12; Gaps 3;

QY 1084 TTTAAGCTTAAGCTGCGCAAGTGTATCTATTATGATGGAACAGATTGAAATCCC 1143  
 DB 3256 TCTGATTTAAAGATCTTGAAGAGATATTTAAAGAGCTAAAGAAATCAAGAACTT 3315  
 QY 1144 AATAAGAGATAGTAGACCTTACTCTGTAAGACATATATGTTTGAAGATTAGC 1203  
 DB 3316 GAAAGTCAATTTTATAGAGATTTAAAGAACTTTGAAAGACAGATATTTTGA 3375  
 QY 1204 GTTTAACTACACAAAATCTATGCAAAATTTATATGCAAAAATTAATAATGAACTTCA 1263  
 DB 3376 GAGAAAAAAGAAATAGAAAAAGATCATTTTGAAAAATTCAGAGAGAGCTGAAGAAATA 3435  
 QY 1264 CAGGTGCTATTTGCTTTAATGCAAGATCTAAATCTCCACAGACTCTGAGATGTGGG 1323  
 DB 3436 AAGATCTTGACAGATATTTAAAGAGATCTTCAATTAAGATTGAAGAAATA 3495  
 QY 1324 AAAACATGACTCCAGCTTTTACACAGAGAGTAATAATACACTCATATTGCAAGTCT 1383  
 DB 3496 AATTTAGAGAGACTACGAAATTTAAAGAGAGGTAGAA-----CATATATTAAGTGT 3549  
 QY 1384 GACCTCTTTAATATCTGTGAACCAAGAGATACCGATCTGACACTTTCTTAAACAT 1443  
 DB 3550 GATGCGCATTTAAAGGTTTGGAAGAGATGATTTAGAGAGATGATTTTAAAGGA 3609  
 QY 1444 ATCAAAAAATTAATGCAAGGTTTACAGGAAAAAGACAGCTTATGATAGTGT 1503  
 DB 3610 AGTATATTTAGACATGTTTAAAGGAGATGTGAATTTAGGGATATGATTAAGAAAGTTTA 3669  
 QY 1504 CTAACTGAGACAAATTCGTGGCGGTACTCAGTTACCATATATTTTCCACTGATAGT 1563  
 DB 3670 GAAGATGTAAACAGCAAACTTTGGAAGAGAGTGAATCTTAAAGATGTTTATCTAGT 3729  
 QY 1564 GCTGAATTAAGATTAAGTAACTAAAGACTATCATGTTTGGAGACATGAATGATAGT 1623  
 DB 3730 GC---ATTAGCATGTAGTAAAGAACAAATGAAGAAAGAAAGCTCAAGACCTAAA 3786  
 QY 1624 ACTTTAGCAGTGTCTAAATCTTGTGAATAGCCTCAAGATAGTAACTCCACAGCTA 1683  
 DB 3787 TTGGAAGAGATATTAATAAGAGAGGTTTAAAGAACCAAGAAAGAAATTAACAAA 3846  
 QY 1684 ACTGACCTGATTTCTTATTCGAAATTAACATTAATATCATCTCTTATTTGAACTCAG 1743  
 DB 3847 AAGAAAGTAAAGTTTGTATTAAGATTAAGAACCAAGATGAATAGTAAAGTTGAA 3906  
 QY 1744 TGGCATCCAGAGATTTAGTTGATATATTCGTATGGAAGATTAAGAAAGATTAATCT 1803  
 DB 3907 ATGAAGATGAAGATTAAGATTAAGATTAAGAAAGATTAAGAAAGATTAAGAAAG 3966  
 QY 1804 GTAACTCATTAATTAACATTGAGAAAAAGCGTACGTGTTTACGTGTGACAGAACTAAA 1863  
 DB 3967 GATTAAGTTGAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 4026









